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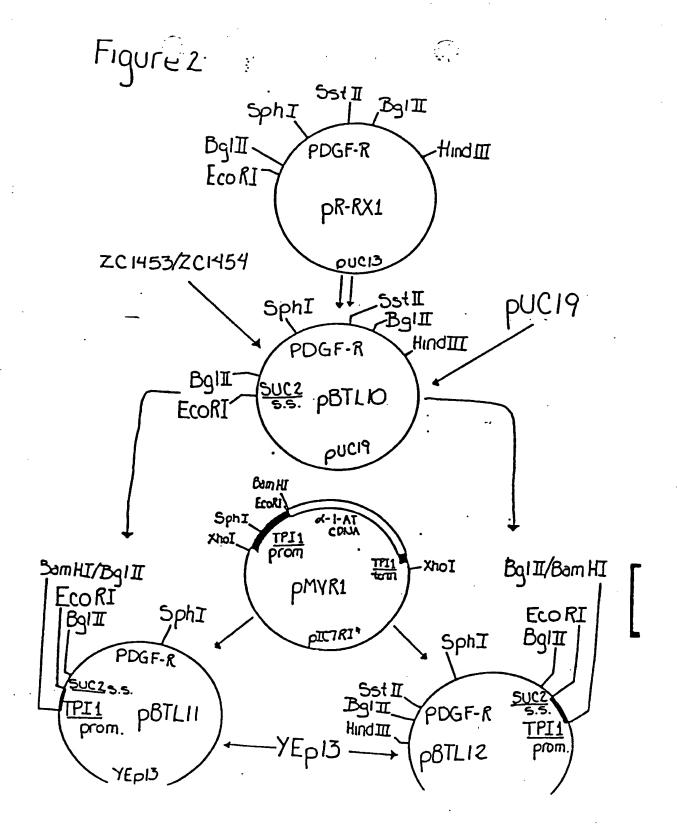
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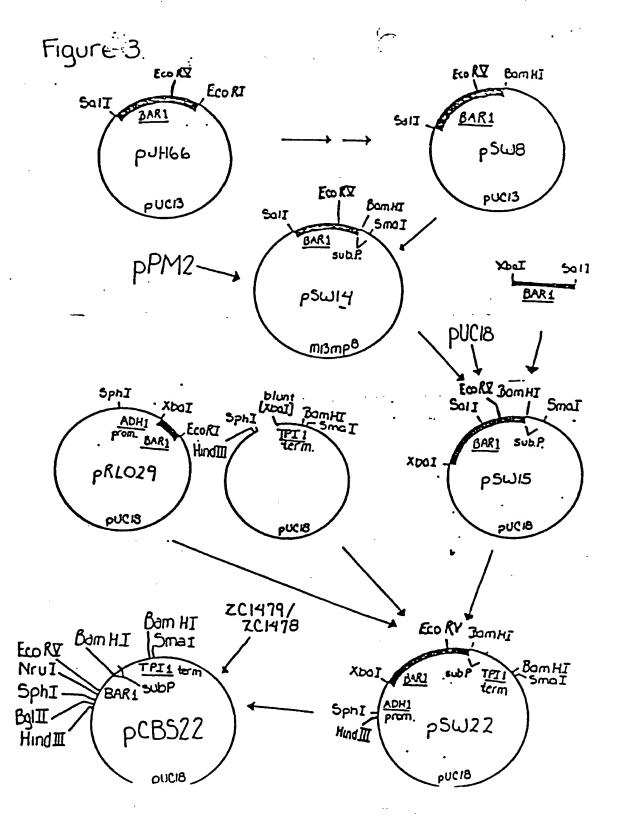
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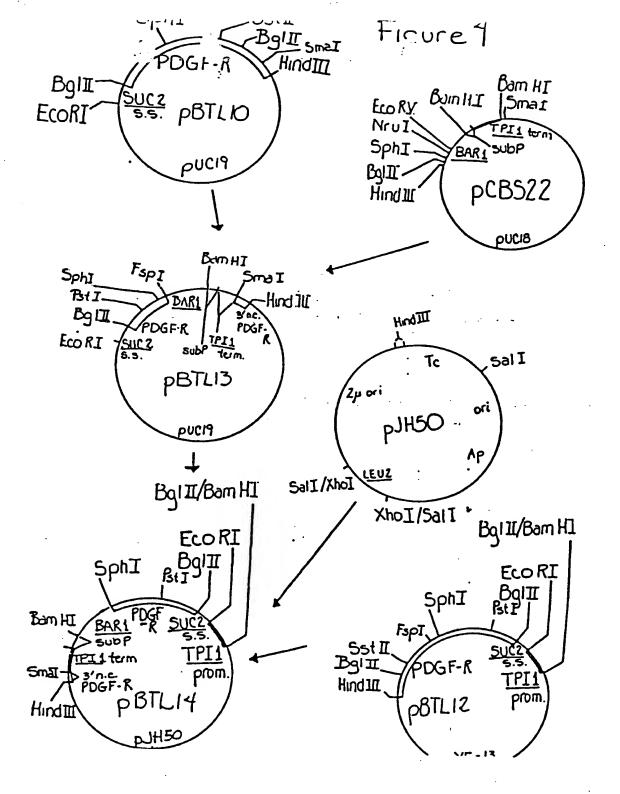
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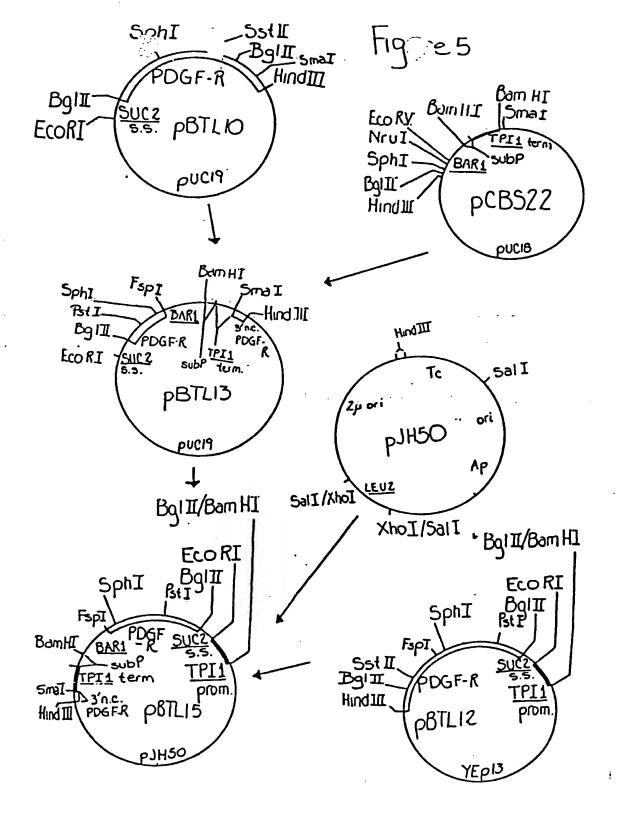
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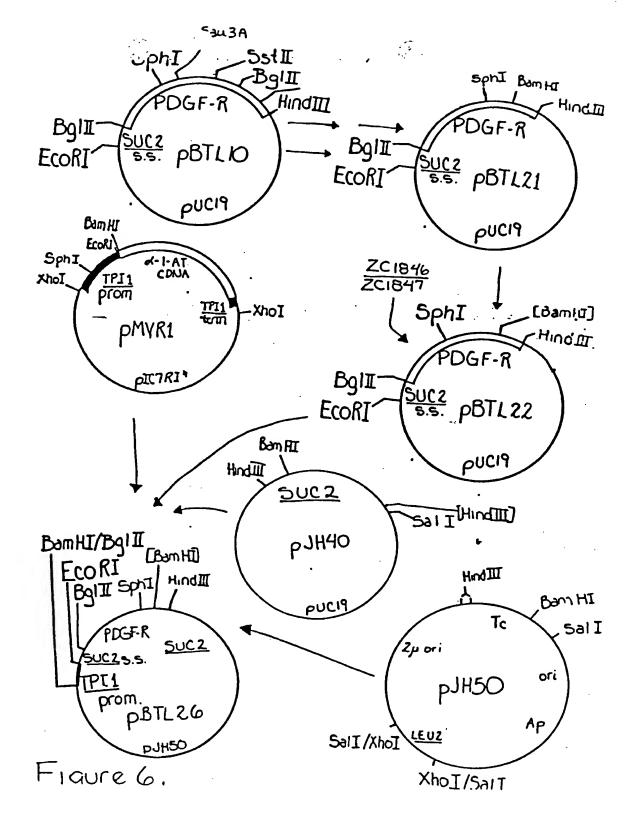
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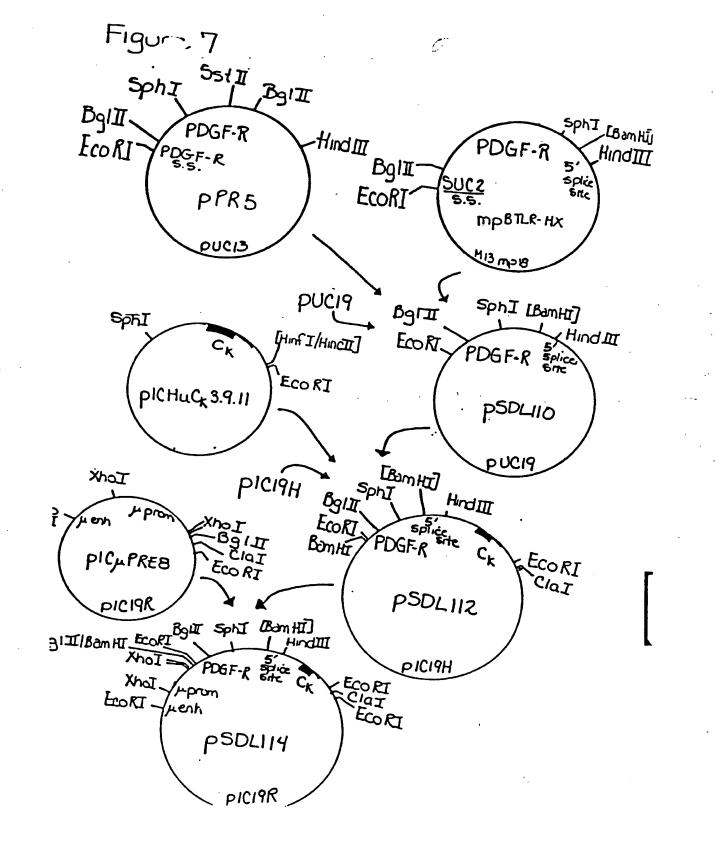
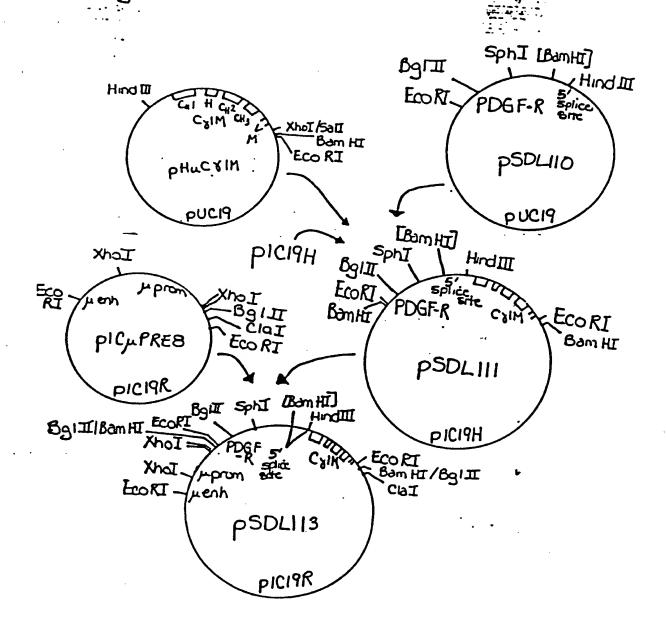


Figure 8



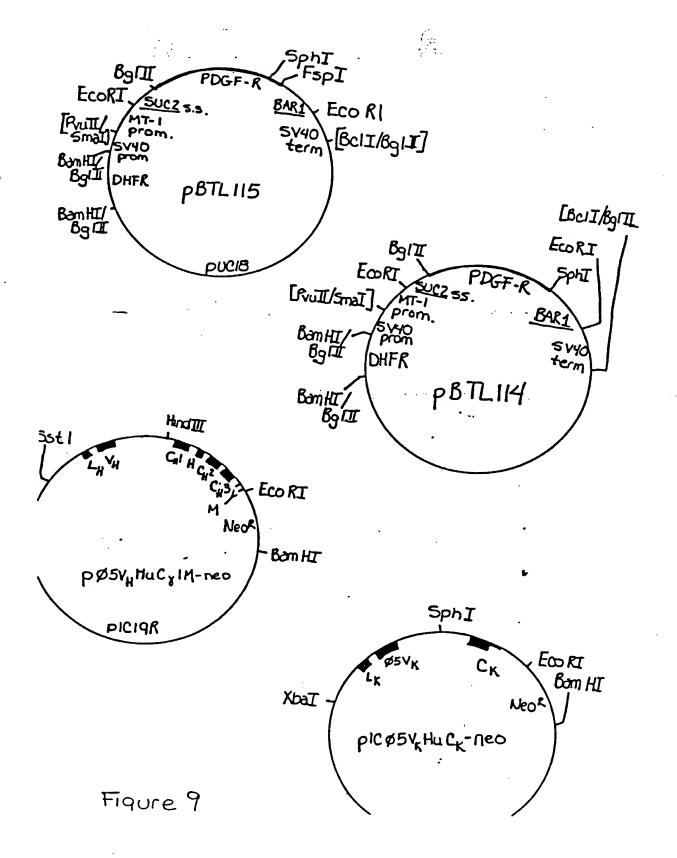
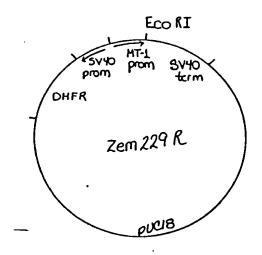
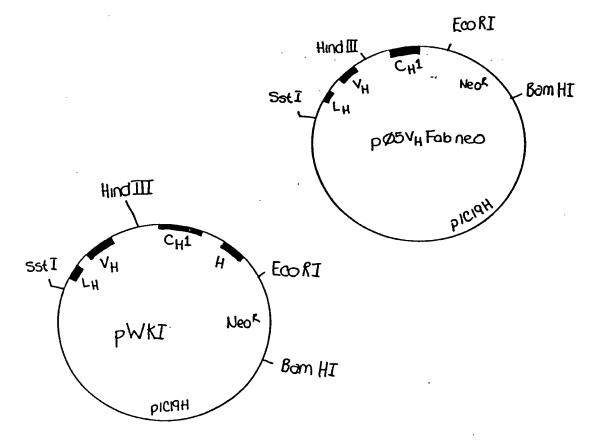


Figure 10





#### FIGURE II

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208	GGGACTTECCATCCCCCTTCCCCCTTCCCCCCTTCCCCCCCCC	-

- 208 GGGACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTCTCACAGGGCTGAGCCTAATCCTCTGCCAG G T S H P A F L V L G C L L T G L S L I L C Q
- 277 CTTTCATTACCCTCTATCCTTCCAAATGAAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTG L s l p s i l p n e n e k v v q l n s s f s l
- 415 ATCAGAAATGAAGAAACAACAGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCGGCC I R N E E N N S G L F V T V L E V S S A S A A
- 553 ATTTACATCTATGTGCCAGACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTAGTCATC
  I Y I Y P D P D Y A P V P L G H T D Y L V I
- 622 GTGGAGGATGATGTTGTCGCATTATACCTTGTCGCACAACTGATCCCGAGACTCCTGTAACCTTACAC V E D D S A I I P C R T T D P E T P V T L H
- 760 CCCTATATCTGTGAGGCCACCGTCAAAGGAAGGAAGTTCCAGACCATCCCATTTAATGTTTATGCTTTA P Y I C E A T V K G K K F Q T I P F H V Y A L
- 829 ANGCANCATCAGAGCTGGATCTAGANATGGANGCTCTTANANCCGTGTATAAGTCAGGGGANCGATT K  $\lambda$  T S E L D L E H E  $\lambda$  L K T V Y K  $_{\rm L}$ S G E T I
- 898 GTGGTCACCTGTGCTGTTTTTAACAATGAGGTGGTTGACCTTCAATGGACTTACCCTGGAGAAGTGAAA V V T C  $\lambda$  V F N N E V V D L Q W T Y P G E V K



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	E	2	•	T	ĸ	5	Y	V	I	L	S	F	E	H	N	G	D	Y	×	D	ĸ	K	Q	A A
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2436	٠,		~																					
2416	6,		C.I.	VC	/CV	GTA	TGI	CCC	CAT	CCI	'AGA	<b>NY</b> C	Gλλ	<b>ryc</b> s	/CC	TTT	TAA	ATA	TTC	CGA	CAT	CCY.	GAG	ATCA
	U	1		T	Q	¥	V	P	M	L	E	R	X	Ē	V	5	K	Y	S	D	I	Q	R	S
																						_		_
2485	CI	CI	AT	GY 1	CC.	TCC	YCC	CTC	ATA	TAA	GAA	GAA	ATC	TAT	GT	[AG/	CTC	λGλ	AGT	CAA	**	CCT	CCT	TTC
	L	Y		D	R	P	λ	S	Y	K	K	K	S	H	L	D	S	E	v	K	N	T.	7.	
																	_	_	-	••	••	_	_	•
2554	Gλ	TG	AT.	WC	TC	λGλ	λGG	CCT	TAC	TTT	ATT	GGA	TIT	GTI	GAC	CT	CAC	CTA	TCA	AGT	TGC	ccc	100	1170
	D	D	1	N	S	E	G	L	T	L	L	D	L	L	S	•	Ŧ	Y	-	v	•••	- E	~~	~~.
											_	_	_	_	_	•	•	•	4	•	~	~	•	n
2623	Gλ	GT	IT.	TTG	CC	TTC.	W	AAA:	TTG	rg T	CCA	CCG	TGA	TCT	GGC	TGC	TCG	CLL	CCT			ccc		1001
	E	F	1	L	λ	S	K	N	Ċ	V	H	R	D	ī.	A	A	P	N	4	T.		300	~~~	~~~
									-	-			_	_			••	••	•	_	_	^	¥	•
2692	λλ	XX:	T	TG	AAC	SAT	CTG	TGA	-1-1-	raci	_	acc	CAG	161	CAT	'C 2 T	~~~	~ .	-		~~.			
	K	I	1	7	K	Ī	Ċ	D	F		1.	3	- B	777	~~	~.	Š	TOV	114	PYV.	CIA	TGT	GTC	GAAA
		_				-	_	-	•	•	-	^		U	-	-	Д	U	3	M	I	V	\$	K
2761	GG	CA	;;;	١٥٥	J-T-1	ملت		~		:TY:	2 h Tr		T	<b>~</b>	~ . ~	~-								
	Ğ	s	1	•	P '	T.	ם ס	V	-~~\ Y		-A.,		100	* ^v	CAG	T	CLL	ICY		CCL	CTA	CYC	CYC	ACTG
	-	_	•	•	-	~	•	•	•	-	n	^	P	Ł	3	T	r	D	H	L	Y	T	T	L

- 2830 AGTGATGTCTGGTCTTATGGCATTCTGCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGGC S D V W S Y G I L L W E I F S L G G T P Y P G
- 2899 ATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGCT H H V D S T F Y N K I K S G Y R H A K P D H A
- 2968 ACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGAGCCCTCCTTTTAC T S E V Y E I N V K C W N S E P E K R P S F Y
- 3037 CACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTG HLSEIVENLLPGQYKKSYEKIHL
- 3106 GACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGGT D F L K S D H P A V A R H R V D S D N A Y I G
- 3244 GCTGACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAG ADSGYIPPDIDPVPEEEDLGK
- 3313 AGGAACAGACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTTC RNRHSSQTSEESAIETGSSSSTF
- 3382 ATCAAGAGAGAGGACGAGACCATTGAAGACATCGACATGATGACGACATCGGCATAGACTCTTCAGAC I K R E D E T I E D I D H H D D I G I D S S D
- L V E D S F L 1089
- 3520 ATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAG
- 3727 AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAA
- 3796 TTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGATTG
- 3934 ATGTAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTTTGAACCTTAAAAGGTACTGGT
- 4003 ACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGTAAAGAATAATAAG

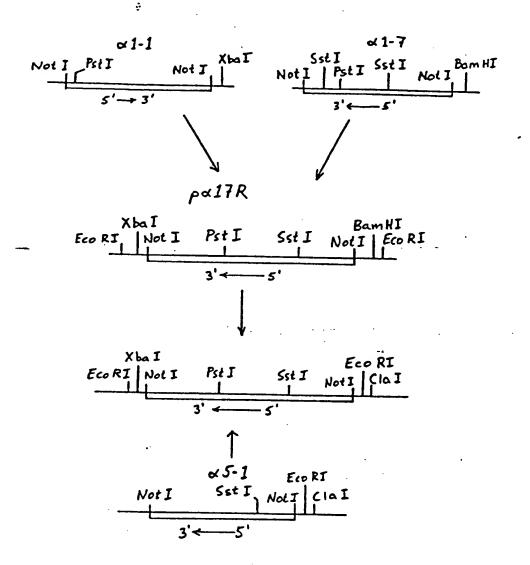


FIGURE 12

1	GGCC	CCT	'C <b>X</b> G	ccc	TGC	TGC	cci	AGC	ACG.	<b>A</b> GC	CTGI	GCT	'CGC	CCI	GCC	CYY	CGC	λGλ	CAG	CCY	GAC	CCA	GG	69
70	GCGG	ccc	CTC	TGG	CGG	CTC	TG	CTC	CTC	CCG	<b>AAG</b> G	АTG	CTI	GGG	GλG	TGA	GGC	GAA	GCT	GGG	CGC	TCC	TC	138
139	TCCC	ста	CAG	CAG	ccc	CCI	TC	CTC	CAT	ccc	rctg	TTC	TCC	TGA	GCC	TTC	λGG	λgc	CTG	CAC	CAG	TCC	TG	207
208	CCTG	TCC	TTC	TAC	TCA	GCT	GT	race	CCA	CTC:	rggg	ACC	λGC	AGT	CTT	тст	GAT	AAC	TGG	GAG	AGG	GCA	СT	276
277	λλGG	AGG	ACT	TCC	TGG	λGG	GGG	GTG/	ACT	GTC	CAGA	GCC	TGG	AAC	TGT	GCC	CAC	ACC	λGA	AGC	CAT	CAG	CA	345
346	GCAA	GGA	CAC																					414
				н	R	L	P	·G	Λ	M	P	λ	L	A	L	K	G	E	L	L	L	L	5	20
415	CTCT				_																			483
	L	L	L	L	L	E	₽	Q	I	8	Q	G	L	V	V	T	P	P	G	₽	E	L	V	43
484	TCCT																							552
	L	N	V	8	. <b>s</b>	T	P	V	L	T	C	8	G	8	λ	P	V	V.	W	E	R	M	S	66
553	CCCA																							621
	Q	E	P	P	Q	B	H	λ	K	λ	Q	D	G	T	P	8	8	V	L	T	L	T	H	89
622	ACCT																							690
	L	T	G	L	D	T	G	E	Y	P	C	T	H	Н	D	8	R	G	L	E	T	D	B	112
691	AGCG																							759
691											TCC P													759 135
	R TATT	K	R CTT	L TCT	Y CAC	I :GGA	P AA1	V	P CTG	D AGA7	P	T	V TCC	G ATG	P	L Agt	P AAC	N Aga	D	A ACA	E GCT	e Ggt	L GG	135 828
	R TATT	K	R CTT	L TCT	Y CAC	I :GGA	P AA1	V	P CTG	D AGA7	P	T	V TCC	G ATG	P	L Agt	P AAC	N Aga	D	A ACA	E GCT	e Ggt	L GG	135
760	R TATT	K CAT	R CTT F	L TCT L	Y CAC T	I GGA E	P AA1 I	V DAA? T	P CTG/ E	D AGAT I	P CAC T	T CAT I	V TCC P	G ATG C	P CCG R	L AGT	P AAC T	N AGA D	D CCC P	A ACA Q	E GCT L	e GGT V	G G V	135 828
760	R TATT P TGAC	K CAT I ACT	R CTT F GCA	L TCT L CGA	Y CAC T	I GGA E	P AAT I AGG	V T T GGG	P CTG/ E	D AGAT I	P CAC T	T CAT I GCC	V TCC P TGT	G ATG C	P CCG R	L AGT V TGA	P AAC T	N AGA D CCA	D CCC P	A ACA Q TGG	E GCT L	E GGT V TTC	L GG V TG	135 828 158
760 829	R TATT P TGAC	K CAT I ACT L	R CTT F GCA H	L TCT L CGA	Y CAC T GAA K	I GGA E .GAA K	P AAT I AGG	V T T GGG!	P CTG/ E ACG/	D AGAT I TTG(	P TCAC T CACT	T CAT I GCC	V TCC P TGT V	G ATG C	P CCG R CTA Y	L AGT V TGA	P AAC T TCA H	N AGA D CCA Q	D CCC P ACG R	A ACA Q TGG	GCT L CTT	ggt V TTC	L GG V TG G	135 828 158 897 181
760 829	R TATT P TGAC T	CAT	R CTT F GCA H	L TCT L CGA E	Y CAC T GAA K CAG	I GGA E GAA K	P AAT I AGG G	V T T GGGI D	P CTG/ E ACG/ V	D AGAT I TTGO A GCAJ	P TCAC T CACT	T CAT I GCC P	V TCC P TGT V	G ATG C C C C C C C C	P CCG R CTA Y	L AGT V TGA D	P AAC T TCA H GGA	N AGA D CCA Q GGT	D CCC P ACG R	A Q TGG G	GCT L SCTT F	ggt V TTC	GG V TG G	135 828 158 897 181
760 829 898	R TATT P TGAC T	CATOL L	R CTT F GCA H TGA	L TCT L CGA B GGA	Y CAC T GAA K CAG	I GGA B GAA K AAG	AATI AGG G	GGS D	P CTG/ E ACG' V CTC	D AGAT I TTG( A ECA)	P TCAC T CACT L	CAT I GCC P	TCC P TGT V	G ATG C C C C P TGG	P CCG R CTA Y GGA	L AGT V TGA D CAG	P AAC T TCA H GGA	N AGA D CCA Q GGT	D CCC P ACG R GGA	ACA Q TGG G TTC	GCTT F	GGT V TTC S TGC	GG V TG G	135 828 158 897 181 966 204
760 829 898	R TATT P TGAC T GTAT I ACTA	CATOL L	R CTT F GCA H TGA E	L TCT L CGA B GGA D	Y CAC T GAA K CAG R ACT	GGA E GAA K AAG S	P AATI AGG G CTA Y	V TAAC T GGG! D ACAT I	P CTG/ E ACG/ V CTCTC C	D AGAT I TTGO A GCAI K	P TCAC T CACT L	T CAT I GCC P CAC T	V TCC P TGT V CAT	G ATG C C C C C C C C C C C C C C C C C C C	P CCG R CTA Y GGA	L AGT V TGA D CAG R	P AAC TCA H GGA B	N AGA D CCA Q GGT V	D CCC P ACG R GGA	A Q TGG G TTC S	GCTT F	GGT V TTC S TGC	GG V TG G	135 828 158 897 181 966 204
760 829 898 967	R TATT P TGAC T GTAT I ACTA	CATOL CTT P	R CTT F GCA H TGA E CTA	L TCT L CGA B GGA D CAG R	Y CAC T GAA K CAG R ACT L	GGA E GAA K AAG S CCA Q	AATI AGG G CTA Y	V TAAC T EGG! D CAT I	P CTG/ E ACG' V CTCC C	D AGAT I TTGC A GCAI K	P CACT L L LAAC T	T CAT I CGC P CAC T	TCC P TGT V CAT I	G C C C C C C C C C C C C C C C C C C C	P CCG R CTA Y GGA D	L AGT. V TGA D CAG R CGC	P AAC T TCA H GGA B AGT V	N AGA D CCA Q GGT V GCA	D CCC P ACG R GGA D GAC	ACA Q TGG G TTC 8	GCTT F TGA D GGT	GGT V TTC S TGC A CCG R	E G V T G G C T Y C C Q	135 828 158 897 181 966 204 1035 227
760 829 898 967	R TATT F TGAC T GTAT I ACTA Y	K CAT ACT CTT CTT TGT TGA	R CTT F GCA H TGA E CTA Y	L TCT L CGA B GGA CAG CAG	Y CAC T GAA K CAG R ACT L CAC	GGA E GGAA K AAG AAG CCA Q	AATI AGG G CTA Y CAT	V TAAC T GGG ACAT I GTC S	P CTG/ E ACG! V CTCTC C	D AGAT I PTGC A GCAT K CCAT I	P CACT L L LAAC T	CAT P CAC T V CGG	V TCC P TGT V CAT CTC S GAA	G ATG C C C C C C T G T G T G T G	CCG R CTA Y GGA D GAA N	L AGT. V TGA D CAG R CGC A	PAACTCAH	N AGA D CCA Q GGT V GCA Q	D CCC P ACG R GGA GAC T	ACA Q TGG G TTGT V	GCTT F CTGA CTGA CGGT V	GGT V TTC S TGC A CCG R	L GG V TG G CT Y CC Q	135 828 158 897 181 966 204 1035 227
760 829 898 967	R TATT P TGAC T GTAT I ACTA Y AGGG	K CAT I ACT P TGT V TGA	R CTT GCA TGA TGA E CTA Y GAA	L TCT L CGA B GGA D CAG R CAT	Y CAC T GAA K CAG R ACT L CAC	GGA E GAA K AAG S CCA Q	P AAAT I AGG G CTA Y GGGT V CAT H	V TAAC T GGG C TGTC C C	P CTGI E ACGT V CCCAT( S GCAT I	D AGAT I TTGC A GCAT K CCAT I	P CACT L AAAC T CAA N CAA I	T CAT I CAC T CGT V	V TCC P TGT V CAT CTC S GAA	G ATG C C C C C C C C C C C C C C C C C C C	P CCCG R CCTA Y CGGA D CGAA N	L AGT V TGA D CAG R CGC A	P AAC TCA H GGA B AGT V	N AGA D CCA Q GGT V GCA Q CTT	D CCC P ACG R GGA D GAC T	A CA Q TGG G S TGT V GTG W	GCTT F TGA TGA TGACT TGA	E GGT V TTC S TGC A CCG R	GG V TG G CT Y CC Q CC P	135 828 158 897 181 966 204 1035 227 1104 250
760 829 898 967	R TATT P TGAC T GTAT I ACTA Y AGGG G	K CAT ACT L CTT F TGT V TGA E	R CTTT P GCA H TGA E CTA Y GGAA N AGAI	L TCT L CGA B GGA D CAG R CAT I	Y CAC T GAAA K CAG R ACT L CAC T TGG	I GGGA E GAA K AAG S CCA Q CCT L	P AAT I AGG G CTA Y GGT V CAT H	V  TAAC  T  GGGA  L  CAT  C  C  C  C  C  C  C  C  C  C  C  C  C	P P P P P P P P P P P P P P P P P P P	D AGAT I TTGO K CCAT I TTGT V	P CACT L AAAC T CAA N CGAT I	T CAT I GCCC P CAC T CGT V CGG GAC	V TCC P TGT V CAT I CTC S GAA N TGA	G ATG C CCCC P TGG G TGT V TGA E	ECCG R CTA Y GGA D GAA N GGT V	L AGT V TGA CAG R CGC A CGC V CTT	P AAC T TCA H GGA E AGT V CAA H	N AGA D CCA Q GGT V GCA Q CTT F	D CCCC P ACG R GGA C T CCGA E GCCC	A ACA Q TGG G TTC S TGT V GTG	E GCT F C GAC T C CCA	E GGT V TTC S TGC A CCG R ATA Y	L GG V TG G CT Y CC Q CC P	135 828 158 897 181 966 204 1035 227 1104 250
760 829 898 967	R TATT P TGAC T GTAT I ACTA Y AGGG G CCCG R	K CATC I ACTC L CTT F TGTC V TGAC E CAAA	R CTT F GCA H TGA E CTA Y GAA N AGA E	L TCT L CGA B GGA D CAG R CAT I	Y CAC T GAA K CAG R ACT L CAC T GG G	EGGAA K AAG S CCA Q CCT L GCG R	P AAAT I AGG G CTA Y CAT H GCT L	V V T GGGA D ACAT I FGTG S C C C C C C C C C C C C C C C C C C	P P CTG/ E ACG/ V CCTCCC C S GCAT(I	D AGAN I I I I I I I I I I I I I I I I I I I	P TCAC T L AAAC T TCAA N TGAT I CGGT V	T GCC P CAC T CGT V CGG G G G CAC T	V TCC P TGT V CAT I CTC S GAA N TGA D	G ATG C CCC P TGG G TGT V TGA E CTT P	P CCCG R CCTA Y GGAA D CGAA N GGT V	L AGT V TGA D CAG R CGC A GGT V	P AAC T TCA H GGA E AGT V CAA N GGA D	N AGA D CCA Q GGT V GCA Q TAT H	D CCC P ACG R GGA D GGA T CCGA E	A ACA Q TGG G TTC S TGT V GTG W	B GCTT F TGA D GGT V	E GGT V TTC S TGC A CCG R ATA Y	E GG V TG G CT Y CC Q CC P CC R	135 828 158 897 181 966 204 1035 227 1104 250 1173 273
760 829 898 967 1036	R TATT P TGAC T GTAT I ACTA Y AGGG G CCCG R	K CATC I ACTC L CTT P TGTC V TGAC E CAACK	R CTT P GCA H TGA E CTA Y GGAA N AGA E CCTC	L TCT L CGA B GGA D CAG R CAT I AAG S GCA	Y CAC T GAA K CAG R ACT L CAC T GAC CAC CAC CAC CAC CAC CAC CAC CAC CAC	I EGGA E E E E E E E E E E E E E E E E E	P AA71 I AGG G CTAY Y CAT H GCT L CAG	V  TANC T  GGGA D  ACAT I  PGTC C  C  C  TGTC C  TGTC C  TGTC C	P CTGI E ACGT V CCCATC CCCATC S GCATC I CCCGI	D D AGAI	P TCAC T L AAAC T TCAA N TGAT I CGGT V	T CAT I GCC P CAC T CGT V CGG G GAC T	V TCC P TGT V CAT I CTC S GAA N TGA D CTC	G ATG C C C C P T G G G T G T T G A E C T T F G G G G G G G G G G G G G G G G G	P CCCG R CCTA Y GGAA N GGAA N CCCT L	L AGT V TGA D CAG R CGC A CGC L CTT CTA	P AAC T TCA H GGA AGT V CAA N GGA C CAC	N AGA D CCA Q GGT V GCA Q CTT F TAT H CTG	D CCC P ACG R GGAC T CCGA E CCC P CCAA	A ACA Q TGG G TTC S TGT V GTG W TTA	B GCTT F TGA D GGT V GGAC T	B GGT V TTC S TGC A CCG R ATA Y CAT I	L GG V TG G CT Y CC Q CC P	135 828 158 897 181 966 204 1035 227 1104 250 1173 273
760 829 898 967 1036	R TATT P TGAC T GTAT I ACTA Y AGGG G CCCG R GCTC S	K CATC I ACTC L CTT F TGTC V TGAC E CAAA K CATC I	R CTT P GCA H TGA E CTA Y GAA A GAA E CCTC L	L TCT L CGA B GGA CAG R CAT I AAG S GCA H	Y CAC T GAA K CAG R ACT L CAC T GG CAT	I EGGA E E GAA K AAG 8 CCA Q CCT L GCG R CCC P	P AATI I AGG G CTA Y GGT V CATI H GCI L CAG	V  TANC T  GGGA D  ACAT I  PGTC C  C  C  C  C  C  C  A	P CTGI E ACGT V C C C C C C C C C C C C C C C C C C	D AGAN I I TTGO A A COMMING WAS A A GOVERNMENT OF A A GOVERNMENT A	P TCAC T L AAAC T TCAA N TGAT I CGGT V TAGA E	T CAT I GCC P CAC T CGT V CGG G G AC T AGA D	V TCC P TGT V CAT I CTC S GAA N TGA D CTC	G ATG C C C P TGG G TGT V TGA E CTT F GGG G	P CCCG R CCTA Y GGAA N GGT V CCCT L	L AGT. V TGA. D CAG. R CGC. A CTT. L CTA. Y	P AAC T CA H GGA AGT V CAA N GGA C CAC T	N AGA D CCA Q GGT V GCA Q CTT F TAT M CTG	D CCC P ACG R GGA D GAC T CGA E	A ACA Q TGG G TTC S TGT V GTG W TTA	B GCT L CTT F TGA D GGC T CCA H	B GGT V TTC S TGC A CCG R ATA Y CAT I GGA E	L GG V TG G CC P CC R GA S	135 828 158 897 181 966 204 1035 227 1104 250 1173 273 1242 296

Fig. 1A

1312	TGGG G	AG) B	V V	rgg( <b>G</b>	CAC T	eact L	ACA Q	lati P	TGC <b>À</b>	TGA E	GCT L	GCA H	TCG R	GAG 8	CCG R	GAC T	ACT L	GCA Q	GGI <b>V</b>	AGT V	GTT F	CGA(	GG À	1380 342
1381	CCTA	CCC P	P P	GCC P	CAC T	TGI V	CCI L	'GTG'	gti P	CAA K	AGA D	CAA N	CCG R	CAC T	CCT L	G G	CGA D	CTC 8	CAG 8	CGC <b>À</b>	TGG G	CGA.	AA I	1449 365
1450	TCGC	CCI L	GTO 8	CAC T	GCG R	CAA N	CGI V	GTO 8	GGA E	GAC T	CCG R	GTA Y	TGT V	GTC 8	AGA E	GCT L	GAC T	ACT L	GGI <b>V</b>	TCG R	CGT V	GAA K	GG V	1518 388
1519	TGGC	AGA B	GG(	CTG(	4998 H	CTA Y	CAC T	CAT M	GCG R	GGC <b>A</b>	CTT F	CCA H	TGA E	GGA D	TGC <b>À</b>	TGA E	GGT <b>V</b>	CCA Q	GCT L	CTC S	CTT P	CCA Q	GC L	1587 411
1588	TACA Q	GA1	KO?	\TGI V	P P	TGT <b>V</b>	CCC R	rdag V	GCI L	GGA E	GCT L	አእG 8	TGA E	GAG 8	CCA H	CCC	TGA D	CAG S	TGG G	gga <b>e</b>	ACA Q	GAC T	λG V	1656 434
1657	TCCG R	CTG C	TC(	TGC G	CCG R	GGG <b>G</b>	CAT M	GCC P	CCA Q	GCC P	GAA N	CAT I	CAT I	CTC W	GTC S	TGC <b>À</b>	CTG C	CAG <b>R</b>	λGλ D	CCI L	CAA K	AAG R	GT C	1725 457
1726	GTCC P	ACG R	TG/ E	GC7 L	GCC P	GCC P	CAC T	GCT L	GCI L	e G	gaa N	CAG 8	TTC S	CGA E	AGA B	GGA B	GAG 8	CCA Q	GCT <b>L</b>	GGA B	GAC T	TAA H	CG V	1794 480
1795	TGAC	GTA Y	CTC W	GG) B	GGA B	GGA B	GC)	GGA B	GTI P	TGA B	GGI <b>V</b>	rod <b>V</b>	GAG 8	CAC T	ACT L	GCG R	TCT L	GCA Q	GCA H	V V	YGGA D	TCG R	GC P	1863 503
1864	CACT	GTC 8	GG1 V	rgce R	CTC C	CAC T	GCI L	GCG R	CAA N	CGC <b>A</b>	TGT <b>V</b>	G G	KODA Q	AGGA D	CAC T	GCA Q	GGA E	GGT <b>V</b>	CAT I	rcgi V	GGI V	GCC P	AC H	1932 526
1933	ACTC 8	CTI L	GC(	CTI P	TAA K	rgdi <b>V</b>	YGGI	YGGI V	rad I	CTC 8	AGC	CAT I	CCI L	'GGC	CCT L	GGT <b>V</b>	GGI <b>V</b>	GCI L	CAC T	CAT I	CAT I	CTC 8	CC L	2001 549
2002	TTAT	CAT I	CC1	rcat I	CAT M	GCT L	TTC	GCA Q	GAA K	GAA K	GCC P	ACG R	KTT Y	CGA E	GAT I	CCG R	ATG W	GAA K	.GG1 <b>V</b>	GAT I	TGA B	GTC S	TG V	2070 572
2071	TGAG	СТС	TG	CGG	CCA	TGA	GTA	CAT	CTA	CGT	'GGA	ccc	CAT	GC)	GCI	GCC	CT)	TGA	CTC	CAC	GTG		GC	2139
2140	TGCC	GCG	GGZ	CCX	GCI	TGI	CT	GGG	ACG	CAC	CCI	'CGG	сто	TGG	GGC	CTI	TGG	GCA	GG1	rgg1	'GGA		CA	2208
2209	CGGC	TCA H	TGC G	CCI L	GAG S	CCA H	TTC S	TCA Q	GGC <b>À</b>	CAC T	GAT M	GAA K	LÀGΊ <b>V</b>	rggc <b>À</b>	CGI V	CAA K	GAT <b>M</b>	GCI L	TAI K	ATC S	CAC T	AGC	CC R	2277 641
2278	GCAG 8	CAG S	TG#	\Gλλ Κ	GCA Q	AGC	CCI L	TAT <b>M</b>	GTC S	GGA E	GCI L	GAA K	GAT I	CAT M	GAG S	TCA H	CCI L	TGG G	GCC P	CCC#	L L	GAA N	.CG V	2346 664
2347	TGGT V	CAA N	CC1	rgti L	YGGG <b>G</b>	GGC <b>À</b>	CTC C	CAC T	CAA K	LAGG G	AGG G	ACC P	CAT I	Y Y	I	CAT I	CAC T	TGA E	GT)	CTC	CCC R	CTA Y	.CG G	2415 687
2416	GAGA D	CCI L	GG1 V	KDD?	CTA Y	CCI L	GC) H	CCC R	CAA N	KAN	ACA H	CAC T	CTI P	rcci L	rgca Q	GCA H	CCA H	CTC S	CG)	KCA,	GCG R	CCG R	CC P	2484 710
2485	CGCC	CAG	CGC	:GGA	GCI	CTA	CAG	CAA	TGC	тст	GCC	CGT	TGC	GCT	rccc	ccı	SCC	CAC	CCI	\TG7	rgt(	CTT	Ġλ	2553 733

2554 CCGGGGAGAGCGACGTGGCTACATGGACATGAGCAAGGACGAGTCGGTGGACTATGTGCCCATGCTGG 2622 GESDGGYMDHSKDESVDYVPHLD756 2623 ACATGAAAGGAGACGTCAAATATGCAGACATCGAGTCCTCCAACTACATGGCCCCTTACGATAACTACG 2691 MKGDVKYADIESSNYMAPYDNYV 779 2692 TTCCCTCTGCCCCTGAGAGGACCTGCCGAGCAACTTTGATCAACGAGTCTCCAGTGCTAAGCTACATGG 2760 PSAPERTCRATLINESPVLSYMD 802 2761 ACCTCGTGGGCTTCAGCTACCAGGTGGCCAATGGCATTGGAGTTTCTGGCCTCCAAGAACTGCGTCCACA 2829 LVGFSYQVANGMBPLASKNCVHR 825 2830 GAGACCTGGCGGCTAGGAACGTGCTCATCTGTGAAGGCAAGCTGGTCAAGATCTGTGACTTTGGCCTGG 2898 DLAARNVLICEGKLVKICDFGLA 848 2899 CTCGAGACATCATGCGGGACTCGAATTACATCTCCAAAGGCAGCACCTTTTTGCCTTTAAAGTGGATGG 2967 RDIMRDSNYISKGSTFLPLKWMA<sup>871</sup> 2968 CTCCGGAGAGCATCTTCAACAGCCTCTACACCACCCTGAGCGACGTGTGGTCCTTCGGGATCCTGCTCT 3036 PESIFNSLYTTLSDVWSFGILLW 894 3037 GGGAGATCTTCACCTTGGGTGGCACCCCTTACCCAGAGCTGCCCATGAACGAGCAGTTCTACAATGCCA 3105 EIPTLGGTPYPELPHNEQPYNAI 917 3106 TCAAACGGGGTTACCGCATGGCCCAGCCTGCCCATGCCTCCGACGAGATCTATGAGATCATGCAGAAGT 3174 KRGYRNAQPAHASDEIYEIMQKC 940 3175 GCTGGGAAGAGTTTGAGATTCGGCCCCCCTTCTCCCAGCTGGTGCTGCTTCTCGAGAGACTGTTGG 3243 WEEKPEIRPPPSQLVLLERLLG 963 3244 GCGAAGGTTACAAAAAGAAGTACCAGCAGGTGGATGAGGAGTTTCTGAGGAGTGACCACCCAGCCATCC 3312 EGYKKYQQVDEFLRSDHPAI L 986 3313 TTCGGTCCCAGGCCCGCTTGCCTGGGTTCCATGGCCTCCGATCTCCCCTGGACACCAGCTCCGTCCTCT 3381 R S Q A R L P G F H G L R S P L D T S S V L Y 1009 TAVQPNEGDNDYIIPLPDPKPEV1032 ADEGPLEGSPSLASSTLNEVNTS1055 3520 CCTCAACCATCTCCTGTGACAGCCCCCTGGAGCCCCAGGACCAGAGCCAGAGCCCAGCTTGAGC 3588 STISCDSPLEPQDEPEPQLEL1078 3589 TCCAGGTGGAGCCGGAGCCAGAGCTGGAACAGTTGCCGGATTCGGGGTGCCCTGCGCCTCGGGCGGAAG 3657 QVEPELEQLPDSGCPAPRAEA1101 EDSFL. 3727 CCAGCATCTCCTGGCCTGGCCTGACCGGGCTTCCTGTCAGCCAGGCTGCCCTTATCAGCTGTCCCCTTC 3795

3865 AGGGGCCGTGACCAGCCTCTGCCTCCAGGGAGGCCAACTGACTCTGAGCCAGGGTTCCCCCAGGGAAC 3933 3934 TCAGTTTTCCCATATGTAAGATGGGAAAGTTAGGCTTGATGACCCAGAATCTAGGATTCTCTCCCTGGC 4002 4003 TGACACGGTGGGGAGACCGAATCCCTCCCTGGGAAGATTCTTGGAGTTACTGAGGTGGTAAATTAACAT 4071 4072 TTTTTCTGTTCAGCCAGCTACCCCTCAAGGAATCATAGCTCTCTCCTCGCACTTTTTATCCACCCAGGA 4140 4141 GCTAGGGAAGAGACCCTAGCCTCCCTGGCTGCTGGCTGAGCTAGGCCTAGCTTGAGCAGTGTTGCCTC 4209 4210 ATCCAGAAGAAAGCCAGTCTCCTCCCTATGATGCCAGTCCCTGCGTTCCCTGGCCCGAGCTGGTCTGGG 4278 4279 GCCATTAGGCAGCCTAATTAATGCTGGAGGCTGAGCCAAGTACAGGACACCCCCAGCCTGCAGCCCTTG 4347 4348 CCCAGGGCACTTGGAGCACACGCAGCCATAGCAAGTGCCTGTGTCCCTGTCCTTCAGGCCCATCAGTCC 4416 4417 TGGGGCTTTTTCTTTATCACCCTCAGTCTTAATCCATCACCAGAGTCTAGAAGGCCAGACGGGCCCCG 4485 4555 CTCTGCATTGGACCTGCTATGAGGCTTTGGAGGAATCCCTCACCCTCTCTGGGCCTCAGTTTCCCCTTC 4623 4624 AAAAAATGAATAAGTCGGACTTATTAACTCTGAGTGCCTTGCCAGCACTAACATTCTAGAGTATTCCAG 4692 4693 GTGGTGCACATTTGTCCAGATGAAGCAAGGCCTATACCCTAAACTTCATCCTGGGGGTCAGCTGGGCTC 4761 4762 CTGGGAGATTCCAGATCACACATCACACTCTGGGGACTCAGGAACCATGCCCCTTCCCCAGGCCCCCAG 4830 4831 CAAGTCTCAAGAACACAGCTGCACAGGCCTTGACTTAGAGTGACAGCCGGTGTCCTGGAAAGCCCCAAG 4899 4900 CAGCTGCCCCAGGGACATGGGAAGACCACGGGACCTCTTTCACTACCCACGATGACCTCCGGGGGTATC 4968 4969 CTGGGCAAAAGGGACAAAGAGGGCAAATGAGATCACCTCCTGCAGCCCACCACTCCAGCACCTGTGCCG 5037 5038 AGGTCTGCGTCGAAGACAGAATGGACAGTGAGGACAGTTATGTCTTGTAAAAGACAAGAAGCTTCAGAT 5106 5176 CCCTGAGGCATGCGCTCCATGGGGGTATGGTTTTGTCACTGCCCAGACCTAGCAGTGACATCTCATTGT 5244 5245 CCCCAGCCCAGTGGGCATTGGAGGTGCCAGGGGAGTCAGGGTTGTAGCCAAGACGCCCCGCACGGGGA 5313 5314 GGGTTGGGAAGGGGGTGCAGGAAGCTCAACCCCTCTGGGCACCAACCCTGCATTGCAGGTTGGCACCTT 5382 5383 ACTTCCCTGGGATCCCCAGAGTTGGTCCAAGGAGGGAGAGTGGGTTCTCAATACGGTACCAAAGATATA 5451 5452 ATCACCTAGGTTTACAAATATTTTTAGGACTCACGTTAACTCACATTTATACAGCAGAAATGCTATTTT 5520 5521 GTATGCTGTTAAGTTTTCTATCTGTGTACTTTTTTTTAAGGGAAAGATTTT 5572

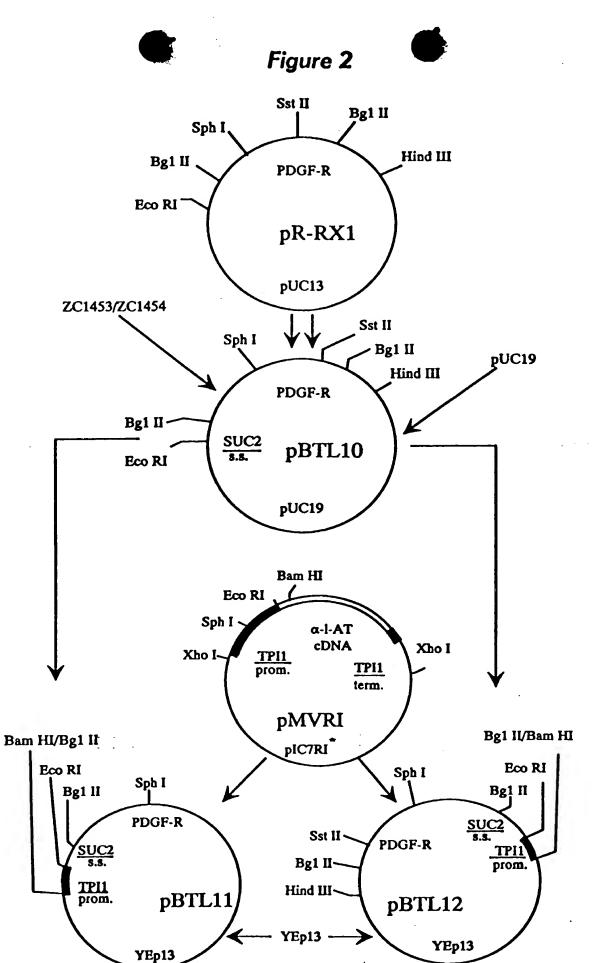


Figure 3

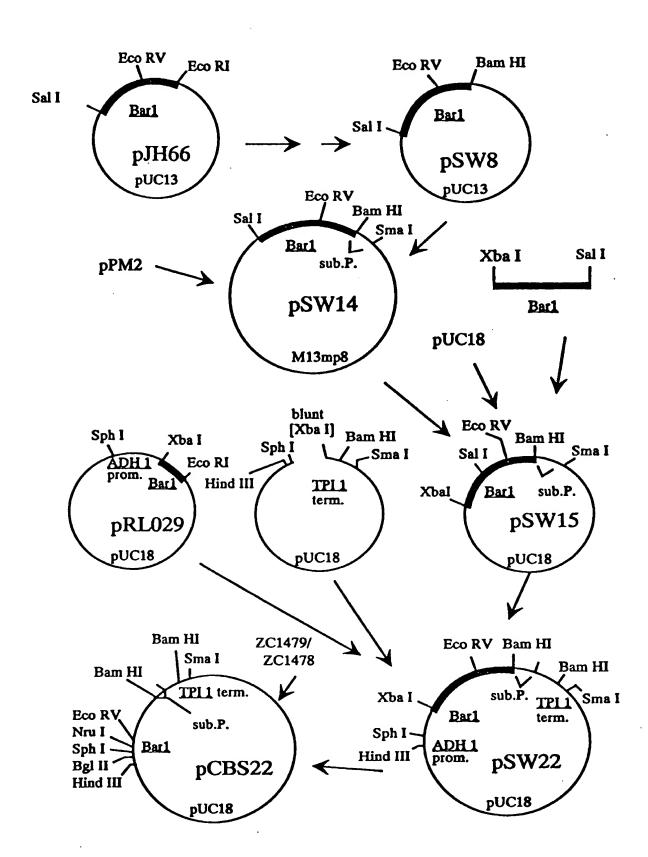


Figure 4

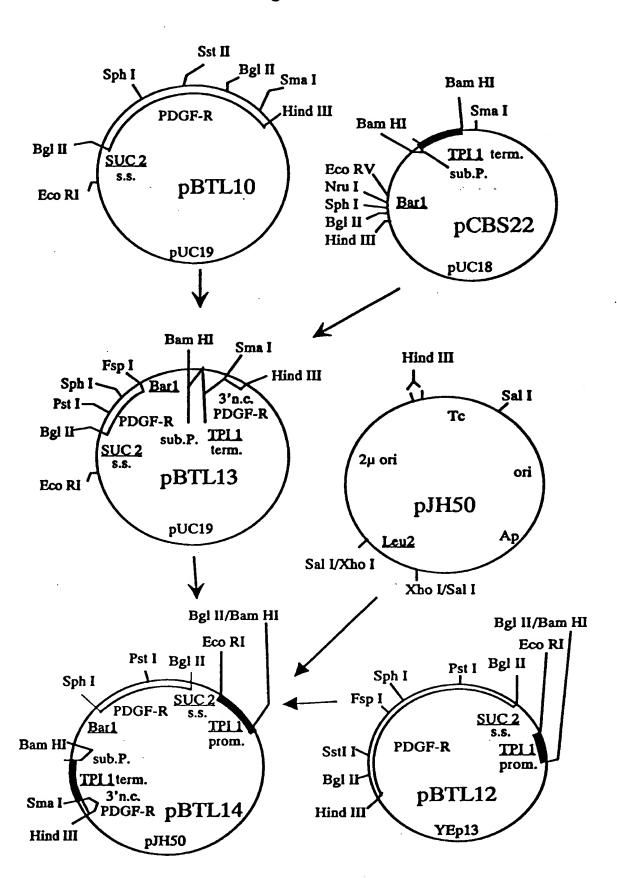


Figure 5

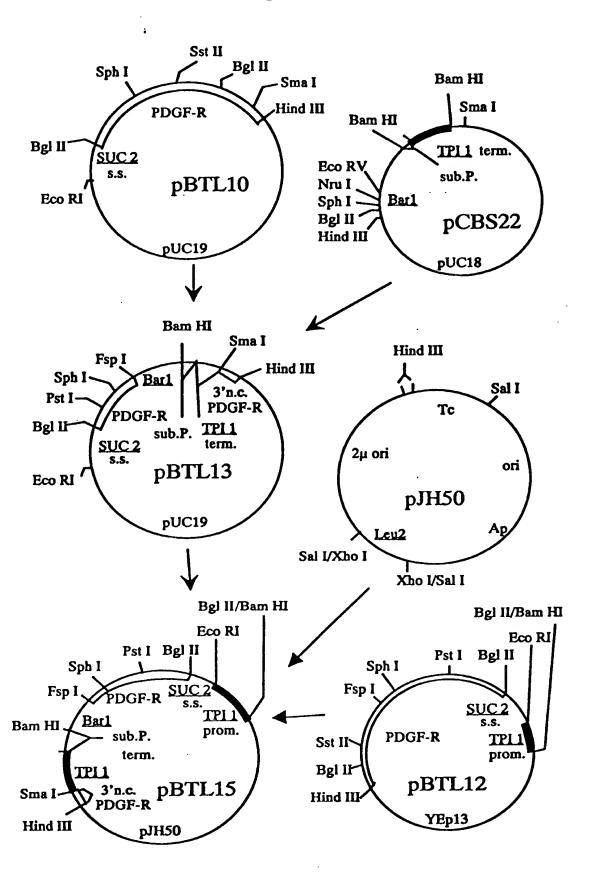


Figure 6

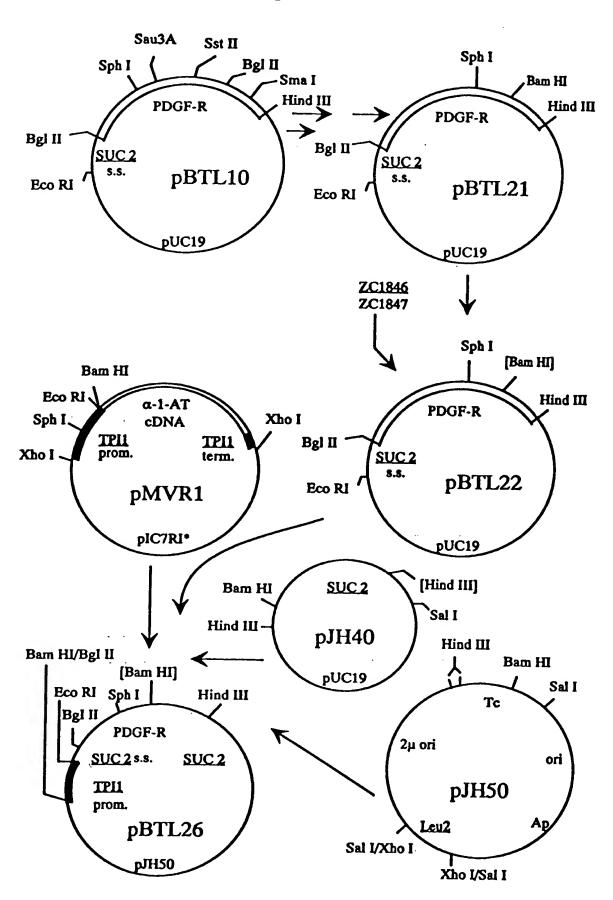


Figure 7

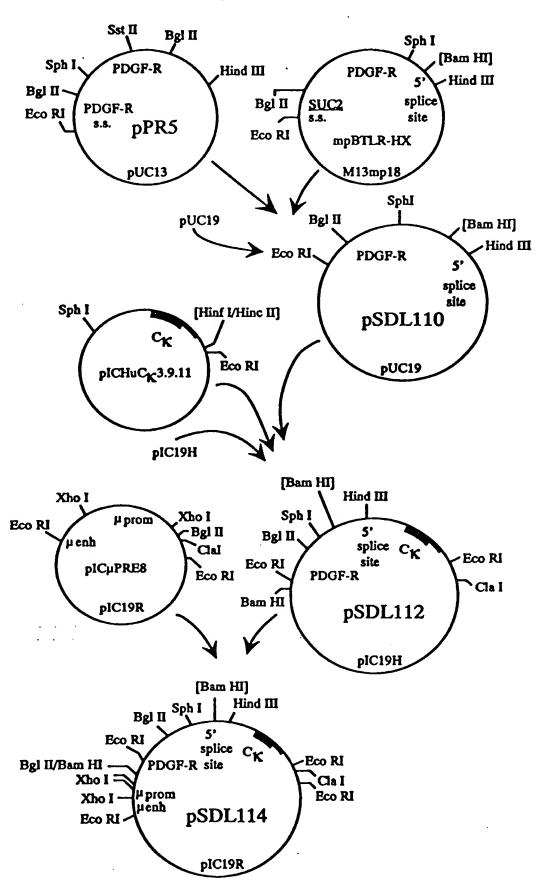


Figure 8

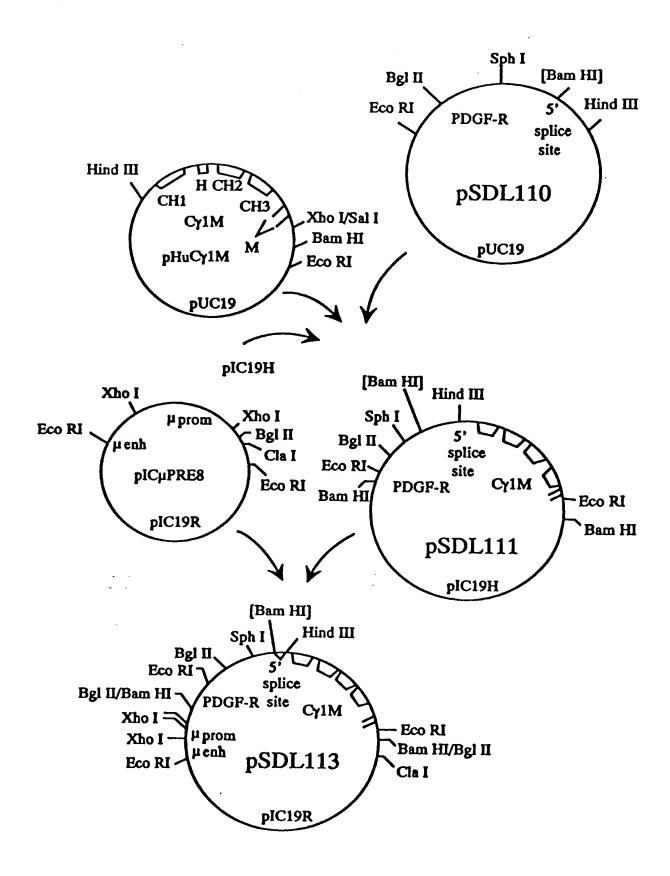


Figure 9

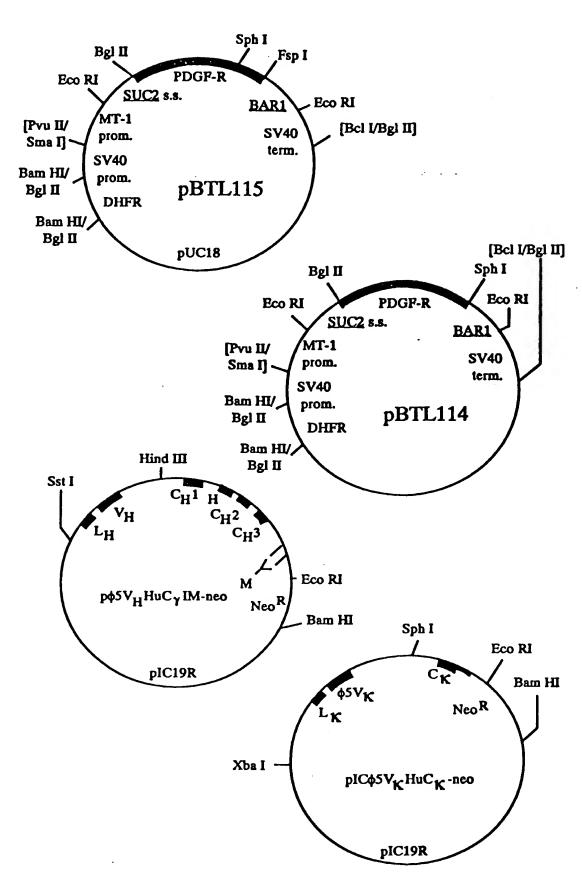
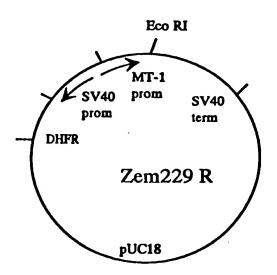
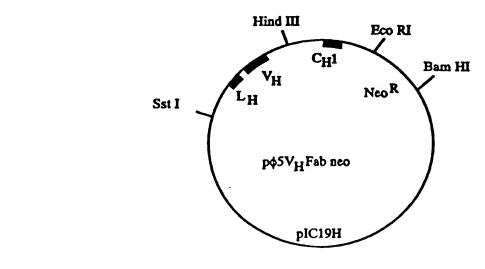
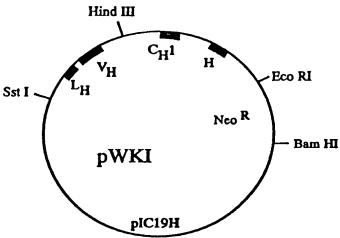


Figure 10







#### Figure 11A

1																							GCCT
70	TO	CTO	CAC	SACC	CAC	CAGO	GA4	GTA	CTC	CCT	TTG	ACC	TCC	GGG	GAG	CTG	CGA	ACC.A	GGT	TAT	ACG	TTG	CTGG
139	TO	GA/	<b>VAA</b> (	atg/	\CA4	ATTO	CTAC	GAA	AAG	SAGC	TAA	AAG	CCG	GA1	rcg@	TGA	CCC		GTT	TCC	CAG	AGC	TATG M 1
208		GAC T																	CCT L				CCAG Q
277		-		ACC P										VGGT V			-		TTC S				TCTG L
346				TGG <b>G</b>																			GGAA E
415	AT I		AAA N	TGA E	AGA E	AAA N	CAA N	CAG S											CAG S				GGCC A
484	_	-		GTT L	-																	<b></b>	GCAC H
553				CTA Y				CCC P										-	GGA D				CATC I
622		GGA E		TGA D	TGA D		TGC A		TAT I	ACC P			CAC T		TGA D	TCC P		-	TCC P	TGT. V			ACAC H
691		-		GGG G												-			GAC(				AGGG G
760	CC P		TAT I																TAA' N			TGC A	TTTA L
B2 <b>9</b>				ATC. S																			GATT I
398				CTG <sup>-</sup>															CCC <sup>-</sup>			-	gaaa K

## Figure 11B

967	GG	CAA	AGG	CAT	CAC	AA:	TAC1	rgg/	VAG/	WAT	CAA	VAG1	rcc(	CAT	CCAT	CAA	ИΠ	GG1	GTA	CAC	т	GAC	CGGTC
		K		I	T	I	Ł	Ε	Ε	I	K	٧	P	S	I	K	L	٧	Y	T	L	T	٧
1036	CC	CGA	GGC	CAC	GGT	GA/	VAGA	<b>ACA</b> 6	STGG	<b>AGA</b>	ATTA	CG/	WT0	STG(	CTGC	CCG	iCC/	\GGC	CTAC	CAG	GGA	GGT	CAAA
	P	Ε	Α	T	٧	K	D	S	G	D	Y	Ε	С	Α	Α	R	Q	À	T	R	Ε	٧	K
1105																							CCAG
	Ε	M	K	K	٧	T	I	S	٧	Н	Ε	K	G	F	I	Ε	I	K	P	T	F	S	Q
1174						CCT									raga	GGT	GCG	GGC	CTA	CCC	ACC	TCC	CAGG
	L	Ε	A	٧	N	L	H	Ε	٧	K	Н	F	٧	٧	Ε	٧	R	A	Y	P	P	P	R
1243																					TGT	-	VAAG
	I	S	W	Ĺ	K	N	N	L	T	L	I	Ε	N	L	T	Ε	I	T	T	D	٧	E	K
1312																			AGA				TATT
	Ι	Q	Ε	Ι	R	Y	R	S	K	Ĺ	K	L	I	R	A	K	Ε	E	D	S	G	Н	Y
1381																							TTCA
	ı	1	٧	Α	Q	N	Ł	U	Α	V	K	S	Y	T	F	Ε	L	L	T	Q	٧	P	S
1450																							TGAA
	S	I	L	D	L	٧	D	D	Н	Н	G	S	T	G	G	Q	T	V	R	С	T	Α	Ε
1519																					-	AAC	TTCC
	G	T	Р	L	Р	D	I	Ε	W	М	I	С	K	D	I	K	K	С	· N	N	E	T	S
1588	TGO	GAC	TAT	Щ	GGC	CAA	CAA	TGT	CTC	AAA	CAT	CAT	CAC	GGA	GAT	CCA	CTC	CCG	AGA	CAG	GAG	TAC	CGTG
	W	1	1	L	Α	N	N	V	S	N	Ι	I	T	Ε	I	Н	S	R	D	R	S	T	٧
1657																		ССТ			GAA	тст	CCTT
	Ε	G	R	٧	T	F	Α	K	٧	Ε	Ε	T	Ι	Α	٧	R	С	Ĺ	Α	K	N	L	Ĺ
1726	GG/	AGC1	GA(	GAA(	CCG	AGA	GCT	GAA	GCT	GGT	GGC <sup>*</sup>	TCC	CAC	ССТ	GCG	TTC	TGA	ACT	CAC	GGT	GGC	TGC	TGCA
	G	A	t	N	K	Ł	L	K	L	٧	Α	P	ſ	L	R	S	E	L	T	٧	Α	Α	Α .
1795	GTO	CCTO	GTO	CTO	STT	GGT	GAT	TGT	GAT	CAT	CTC	ACT	TAT	TGT	CCT	GGT	TGT	CAT					ACCG
	V	L	٧	L	L	V	I	V	I	I	S	L	I	٧	L	٧	٧	I	W	K	Q	K	Ρ

### Figure 11C

1864		IGG }	TA Y	TGA E	'AA' I	TTC R	GCT W	GGA R	NGGG V	TCA I	ATTO E	IAAI S	CAA	TCA S	AGC(	CC( P	GA D	TGG	ACA H	ATG/	۸TA4 Y	ATA <sup>*</sup>		TG1	GGA
1933																									
1900	P	)	M	Q	L	P	Y	0	S	R	l W	l E	F	P	) F	R	D D	G	AC I	.V	L	G		GG I V	CTT
2002	G	GG	TC <sup>-</sup> S	TGG G	AG( A	CGT F	TTG G	GGA K	AGG V	TGG V	TTG E	AAG G	GAA T	CAG	CCT	ΓΑΊ Υ	rgg.	ATT	AAC	) (2)	GTC S	\ \ \ \	VACC	TGT	CAT(
2071	Α	AA(	GΠ	rgc	AG1	ΓGΑ	4GA	TGC	TAA	AAC	CCA	CGG	CCA	GAT	CC/	<b>∆</b> GT	GA.	<b>4</b> 44	AC <i>A</i>	VAG(	CTC1	CAT	GTO	TGA	ACTO
	K	١	/	A	٧	K	M	L	K	P	T	Α	R	S		5	Ε	K	Q	A	L	M	S	E	L
2140	A K	AG/	ATA [	M M	GAC T	TC/ H	ACC.	TGG G	GGC P	CAC. H	ATT L	TGA N	ACA I	TTG V	TAA N	VAC I	TT( L	GCT L	GGG G	AGC A	CTC C	CAC T	CAA K	GTC S	AGG( G
2209	C	CC#	ΛΠ [	TA Y	CAT I	CAT	CA(	CAG. F	AGT/ Y	ATTO C	GCT F	TCT.	ATG	GAG	ΑΤΤ	TG	GT(	CAA N	CTA	П	GCA H	TAA	GAA N	TAG R	GGAT D
2278																				_	• •		•••	••	TGAT
	S	F	•	L	S	H	Н	P	Ε	K	P	K	K	Ε	L		D	I	F	G	L	N		A	
2347	G/ F	۸۸۸ S	GC	ACA T	ACG R	GAG S	CTA Y	ATG V	TTA <sup>-</sup>	П	TAT	CTT	TTG/	AAP N	ACA N	ΑT	GG1	[GA	CTA	CAT	GGA D	CAT	GAA	GCA	GGCT
2416																								•	
	D	T		T	Q	Y	V	P	M	L	E	R	K	E	V		S	K	Y	S	D	I	Q	AG R	ATCA S
2485	CT I	CT.	ΑT	GA1 D	CG R	TCC	AGC A	CTC	ATA: V	ATA/	AGA/	AGA/	)TAV	TAT	ΓGΤ	TA	GAC	TCA	4GA	AGT	CAA K	AAA	ССТ	ССТ	TTCA
2554																							_	_	_
2334	D	D	1	N	S	E	G	L	T	L	L	D	L	L	S	GC 1	IIC F	AU( T	ZIA Y	Q Q	AG I				AATG M
2623	GA	GT E	П	TTG	GC1	ITC.		AAA	ΩŢG	TGT	CCA	CCG	TGA	TCT	rgg(	СТ	GCT	CGC	CAA	CGT	ССТ	ССТО	GGC/	ACA/	AGGA
2602																					L			•	
2692	K	I	1	រ ៤ /	AAU <b>K</b>	I I	C	D D	F	G	L	GGC A	CAG R	AGA D	I	TC/	ATG 1	CAT H	GAT D	FTC( S	GAA( N	CTAT Y	rgte V	STCC S	BAAA K
2761	GG	CAG	T.	(CC	П	СТО	ecc.	CGT	GAA	GTG	GAT	GGC	TCC	TGA	GA(	GC/	\TC	Ш	GA(	CAAC	ССТС	CTAC	CACC	ACA	CTG
	u	3	- 1	·	Γ _	L	۲	٧	K	W	M	Α	P	E	S	]		F	D	N	L	Y	T	T	L

#### Figure 11D

2830	AGTGATGTCTGGTCTTATGGCATTCTGCTCTGGGAGATCTTTTCCCTTGGTGGCACCCCTTACCCCGCS D V W S Y G I L L W E I F S L G G T P Y P G	GC.
2899	ATGATGGTGGATTCTACTTTCTACAATAAGATCAAGAGTGGGTACCGGATGGCCAAGCCTGACCACGGM M V D S T F Y N K I K S G Y R M A K P D H A	CT
2968	ACCAGTGAAGTCTACGAGATCATGGTGAAATGCTGGAACAGTGAGCCGGAGAAGAGACCCTCCTTTTA T S E V Y E I M V K C W N S E P E K R P S F Y	AC
3037	CACCTGAGTGAGATTGTGGAGAATCTGCTGCCTGGACAATATAAAAAGAGTTATGAAAAAATTCACCTH L S E I V E N L L P G Q Y K K S Y E K I H L	ΓG
3106	GACTTCCTGAAGAGTGACCATCCTGCTGTGGCACGCATGCGTGTGGACTCAGACAATGCATACATTGCDFLKSDHPAVARMRVDSDNAYIG	SΤ
3175	GTCACCTACAAAAACGAGGAAGACAAGCTGAAGGACTGGGAGGGGTGGTCTGGATGAGCAGAGACTGAGVTYKNEEDKLKDWEGGLDEQRLS	GC
3244	GCTGACAGTGGCTACATCATTCCTCTGCCTGACATTGACCCTGTCCCTGAGGAGGAGGACCTGGGCAAADSGYIIPLPDIDPVPEEEDLGK	4G
3313	AGGAACAGACACAGCTCGCAGACCTCTGAAGAGAGTGCCATTGAGACGGGTTCCAGCAGTTCCACCTRNRHSSQTSSSSSTFF	
3382	ATCAAGAGAGAGACGACATTGAAGACATCGACATGATGGACGACATCGGCATAGACTCTTCAGI K R E D E T I E D I D M M D D I G I D S S D	AC
3451	CTGGTGGAAGACAGCTTCCTGTAACTGGCGGATTCGAGGGGTTCCTTCC	<b>3</b> G
3520	ATCCCGTTCAGAAAACCACTTTATTGCAATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAG	4G
	AAGTTCCCAGCCAAGGGCCTCGGGGAGCGTTCTAAATATGAATGA	
3658	GTCAGTGTTGCCTCTTGCAATGCCTCAGTAGCATCTCAGTGGTGTGTGAAGTTTGGAGATAGAT	
3727	AGGGAATAATAGGCCACAGAAGGTGAACTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAGACAC	
3796	TTTATACTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCAAGGCTGTGTTTAGAT	
3865 3934	TATTAACTATCTTCTTTGGACTTCTGAAGAGACCACTCAATCCATCC	
4003	ACTATAGCATTTTGCTATCTTTTTTAGTGTTAAAGAGATAAAGAATAATAAG	<b>3</b> (
7000	NOTATIONAL ELIGINATION ELITERATED LA CONTRACTOR DE LA CON	

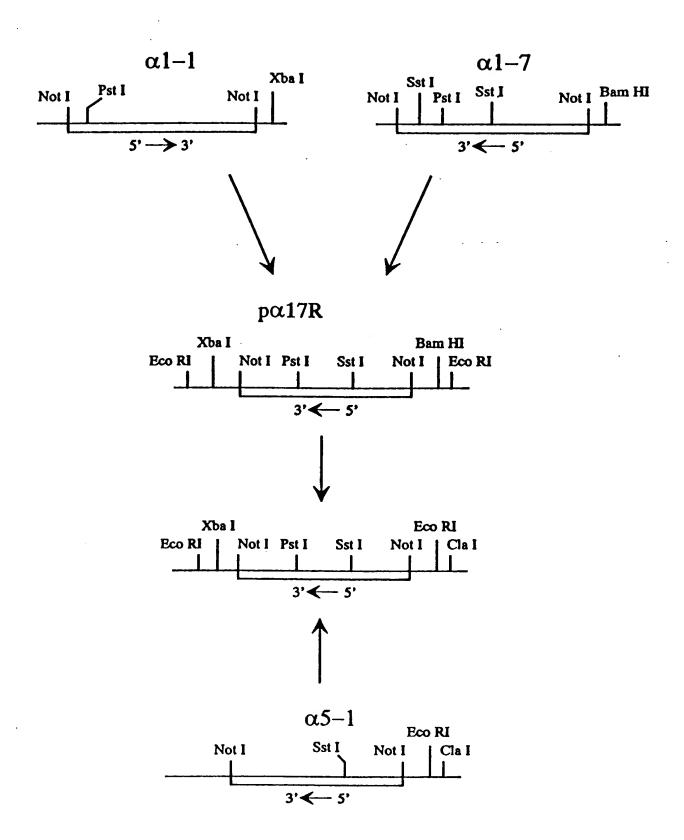


Figure 12